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RAW SEQUENCE LISTING   DATE: 09/03/2002
PATENT APPLICATION: US/09/509,738C   TIME: 15:27:32

Input Set : A:\2186PB-1.ST25.txt
Output Set: N:\CRF4\09032002\I509738C.raw

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 3 <110> APPLICANT: Blatt, Michael
 4        Leyman, Barbara
 6 <120> TITLE OF INVENTION: Protein Involved in Abscisic Acid Signalling
 8 <130> FILE REFERENCE: 2186PB-1
10 <140> CURRENT APPLICATION NUMBER: 09/509,738C
11 <141> CURRENT FILING DATE: 2000-05-24
13 <160> NUMBER OF SEQ ID NOS: 44
15 <170> SOFTWARE: PatentIn version 3.0
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 1205
19 <212> TYPE: DNA
20 <213> ORGANISM: Nicotiana tabacum
22 <220> FEATURE:
23 <221> NAME/KEY: CDS
24 <222> LOCATION: (18)..(917)
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29                      1               5                   10
31 ttc aga gct gac gat caa tcg gac tct cac gcc ata gaa atg gga gac     98
32 Phe Arg Ala Asp Asp Gln Ser Asp Ser His Ala Ile Glu Met Gly Asp
33             15                  20                  25
35 att act ggc gga gtc aat ctc gac aaa ttc ttc gaa gat gtt gaa gcc   146
36 Ile Thr Gly Gly Val Asn Leu Asp Lys Phe Phe Glu Asp Val Glu Ala
37          30                  35                  40
39 att aaa gac gaa ctc aaa ggc ctc gag aaa atc tat tcc caa ctc caa   194
40 Ile Lys Asp Glu Leu Lys Gly Leu Glu Lys Ile Tyr Ser Gln Leu Gln
41       45                  50                  55
43 tct tcc cat gaa aaa agc aag act ctt cac aac gct aaa gcc gtt aaa   242
44 Ser Ser His Glu Lys Ser Lys Thr Leu His Asn Ala Lys Ala Val Lys
45 60                  65                  70                  75
47 gat cta aga tcc aac atg gat aat gac gtt tcc atg gca ttg aag aaa   290
48 Asp Leu Arg Ser Asn Met Asp Asn Asp Val Ser Met Ala Leu Lys Lys
49                  80                  85                  90
51 gcc aaa ttc atc aaa gtt cgt ctc gaa gcc tta gac aga tca aat gca   338
52 Ala Lys Phe Ile Lys Val Arg Leu Glu Ala Leu Asp Arg Ser Asn Ala
53             95                  100                 105
55 gcg aat cga agc ctc cct gga tgt gga ccc gga agt tca tct gac agg   386
56 Ala Asn Arg Ser Leu Pro Gly Cys Gly Pro Gly Ser Ser Ser Asp Arg
57          110                 115                 120
59 acg aga act tca gtt gtg aac gga tta agg aag aaa ctt caa gag tca   434
60 Thr Arg Thr Ser Val Val Asn Gly Leu Arg Lys Lys Leu Gln Glu Ser
61       125                 130                 135
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 63 atg aat cag ttc aac gag cta agg caa aag atg gca tct gaa tat agg      482
 64 Met Asn Gln Phe Asn Glu Leu Arg Gln Lys Met Ala Ser Glu Tyr Arg
 65 140             145             150             155
 67 gaa aca gtt caa cga cga tat tat acc gtc aca gga gaa aat cct gat      530
 68 Glu Thr Val Gln Arg Arg Tyr Tyr Thr Val Thr Gly Glu Asn Pro Asp
 69             160             165             170
 71 gaa gca gtt ctt gat aca ctc ata tct aca ggt caa agt gag acg ttc      578
 72 Glu Ala Val Leu Asp Thr Leu Ile Ser Thr Gly Gln Ser Glu Thr Phe
 73             175             180             185
 75 ttg caa aag gca att caa gag caa ggg aga gga caa gtg atg gat aca      626
 76 Leu Gln Lys Ala Ile Gln Glu Gln Gly Arg Gly Gln Val Met Asp Thr
 77             190             195             200
 79 gtt atg gaa att caa gaa agg cat gaa gct gtg aag gaa ttg gag agg      674
 80 Val Met Glu Ile Gln Glu Arg His Glu Ala Val Lys Glu Leu Glu Arg
 81     205             210             215
 83 aat ttg aaa gaa ttg cat caa gta ttc ttg gac atg gct gtt ttg gtt      722
 84 Asn Leu Lys Glu Leu His Gln Val Phe Leu Asp Met Ala Val Leu Val
 85 220             225             230             235
 87 gaa agt caa gga gct caa ctt gat gat att gag agc caa gtg aat agg      770
 88 Glu Ser Gln Gly Ala Gln Leu Asp Asp Ile Glu Ser Gln Val Asn Arg
 89             240             245             250
 91 gct aat tcc ttc gtt aga ggg ggt gct cag caa ctg caa gtg gca agg      818
 92 Ala Asn Ser Phe Val Arg Gly Gly Ala Gln Gln Leu Gln Val Ala Arg
 93             255             260             265
 95 aag cac cag aag aac act aga aaa tgg act tgt ttt gct att att ctt      866
 96 Lys His Gln Lys Asn Thr Arg Lys Trp Thr Cys Phe Ala Ile Ile Leu
 97             270             275             280
 99 ctg ctt atc atc att ttg gtg gtg gtt ctt tct att cag cca tgg aaa      914
100 Leu Leu Ile Ile Ile Leu Val Val Val Leu Ser Ile Gln Pro Trp Lys
101     285             290             295
103 aaa tgagaatttg tctatggtca aaggtcttct ggtggacccc ttcaatgttt      967
104 Lys
105 300
107 tgaatattct aaattttat attttattat tttagccatg cttattattt tgtgttattt     1027
109 tggatttttt ttttgttttt aatgtgggga agagtaaact ggatgggggt ccatgtgcta     1087
111 tttagagaaa tacttgggag ttctctttttt gtaattattg ctgtatttag agtataattc     1147
113 tttttctata ttgttggcag gttaatttgt ttgtttgatt atattctcat ttagattt     1205
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117 <211> LENGTH: 300
118 <212> TYPE: PRT
119 <213> ORGANISM: Nicotiana tabacum
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128             20             25             30
131 Asn Leu Asp Lys Phe Phe Glu Asp Val Glu Ala Ile Lys Asp Glu Leu
132             35             40             45
135 Lys Gly Leu Glu Lys Ile Tyr Ser Gln Leu Gln Ser Ser His Glu Lys
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Input Set : A:\2186PB-1.ST25.txt
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136     50                   55                  60
139 Ser Lys Thr Leu His Asn Ala Lys Ala Val Lys Asp Leu Arg Ser Asn
140 65                   70                  75                  80
143 Met Asp Asn Asp Val Ser Met Ala Leu Lys Lys Ala Lys Phe Ile Lys
144                  85                  90                  95
147 Val Arg Leu Glu Ala Leu Asp Arg Ser Asn Ala Ala Asn Arg Ser Leu
148                  100                 105                 110
151 Pro Gly Cys Gly Pro Gly Ser Ser Ser Asp Arg Thr Arg Thr Ser Val
152        115                 120                 125
155 Val Asn Gly Leu Arg Lys Lys Leu Gln Glu Ser Met Asn Gln Phe Asn
156      130                 135                 140
159 Glu Leu Arg Gln Lys Met Ala Ser Glu Tyr Arg Glu Thr Val Gln Arg
160 145                 150                 155                 160
163 Arg Tyr Tyr Thr Val Thr Gly Glu Asn Pro Asp Glu Ala Val Leu Asp
164                  165                 170                 175
167 Thr Leu Ile Ser Thr Gly Gln Ser Glu Thr Phe Leu Gln Lys Ala Ile
168                  180                 185                 190
171 Gln Glu Gln Gly Arg Gly Gln Val Met Asp Thr Val Met Glu Ile Gln
172        195                 200                 205
175 Glu Arg His Glu Ala Val Lys Glu Leu Glu Arg Asn Leu Lys Glu Leu
176      210                 215                 220
179 His Gln Val Phe Leu Asp Met Ala Val Leu Val Glu Ser Gln Gly Ala
180 225                 230                 235                 240
183 Gln Leu Asp Asp Ile Glu Ser Gln Val Asn Arg Ala Asn Ser Phe Val
184                  245                 250                 255
187 Arg Gly Gly Ala Gln Gln Leu Gln Val Ala Arg Lys His Gln Lys Asn
188        260                 265                 270
191 Thr Arg Lys Trp Thr Cys Phe Ala Ile Ile Leu Leu Leu Ile Ile Ile
192        275                 280                 285
195 Leu Val Val Val Leu Ser Ile Gln Pro Trp Lys Lys
196      290                 295                 300
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200 <211> LENGTH: 1334
201 <212> TYPE: DNA
202 <213> ORGANISM: Arabidopsis thaliana
204 <220> FEATURE:
205 <221> NAME/KEY: CDS
206 <222> LOCATION: (77)..(991)
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211 atttttcgaa ttttaa atg aac gat ttg ttt tcc agc tca ttc tct cgc ttc     112
212               Met Asn Asp Leu Phe Ser Ser Ser Phe Ser Arg Phe
213                1                5                   10
215 cgc agc gga gaa cca tcc cct cgc cga gac gtt gcc ggc ggt ggc gac      160
216 Arg Ser Gly Glu Pro Ser Pro Arg Arg Asp Val Ala Gly Gly Gly Asp
217       15                  20                  25
219 gga gtt cag atg gcg aat ccc gcg gga tca acc ggt ggt gtg aac ctc      208
220 Gly Val Gln Met Ala Asn Pro Ala Gly Ser Thr Gly Gly Val Asn Leu
221      30                  35                  40
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223 gac aag ttc ttc gaa gat gtt gaa tct gtg aaa gaa gag cta aag gag      256
224 Asp Lys Phe Phe Glu Asp Val Glu Ser Val Lys Glu Glu Leu Lys Glu
225 45               50                55                60
227 cta gat cgg ctc aac gaa aca ctc tct tca tgt cac gag cag agc aag      304
228 Leu Asp Arg Leu Asn Glu Thr Leu Ser Ser Cys His Glu Gln Ser Lys
229              65                70                75
231 acg ctt cac aat gct aaa gcc gtt aaa gat ctc cgg tct aaa atg gac      352
232 Thr Leu His Asn Ala Lys Ala Val Lys Asp Leu Arg Ser Lys Met Asp
233              80                85                90
235 ggt gac gtt gga gtc gcg ttg aag aag gcg aag atg att aaa gtt aaa      400
236 Gly Asp Val Gly Val Ala Leu Lys Lys Ala Lys Met Ile Lys Val Lys
237           95                100                105
239 ctc gag gcg cta gat cgt gcc aat gct gct aat cgg agt ctc cct ggc      448
240 Leu Glu Ala Leu Asp Arg Ala Asn Ala Ala Asn Arg Ser Leu Pro Gly
241     110               115               120
243 tgt gga cct ggt tct tcc tcc gat cga acc agg acc tct gtc ctc aat      496
244 Cys Gly Pro Gly Ser Ser Ser Asp Arg Thr Arg Thr Ser Val Leu Asn
245 125               130               135               140
247 ggt ctc agg aag aaa ttg atg gac tct atg gat agt ttc aac cga ttg      544
248 Gly Leu Arg Lys Lys Leu Met Asp Ser Met Asp Ser Phe Asn Arg Leu
249                   145               150               155
251 agg gag ctt atc tcg tcc gag tat aga gaa act gta cag agg agg tac      592
252 Arg Glu Leu Ile Ser Ser Glu Tyr Arg Glu Thr Val Gln Arg Arg Tyr
253              160               165               170
255 ttc acc gtc acc ggc gag aat ccg gat gaa cga acc cta gat cga ctg      640
256 Phe Thr Val Thr Gly Glu Asn Pro Asp Glu Arg Thr Leu Asp Arg Leu
257         175               180               185
259 att tcc act gga gag agt gag aga ttc ttg cag aaa gca ata caa gaa      688
260 Ile Ser Thr Gly Glu Ser Glu Arg Phe Leu Gln Lys Ala Ile Gln Glu
261     190               195               200
263 caa gga aga gga agg gtg tta gac acc att aac gag att caa gaa agg      736
264 Gln Gly Arg Gly Arg Val Leu Asp Thr Ile Asn Glu Ile Gln Glu Arg
265 205               210               215               220
267 cat gat cgc gtt aaa gac att gag aag aat ctc agg gag ctt cac cag      784
268 His Asp Arg Val Lys Asp Ile Glu Lys Asn Leu Arg Glu Leu His Gln
269                   225               230               235
271 gtg ttt cta gac atg gcc gtg ctg gta gag cac cag gga gct cag ctt      832
272 Val Phe Leu Asp Met Ala Val Leu Val Glu His Gln Gly Ala Gln Leu
273              240               245               250
275 gat gac atc gag agt cat gtg ggt cga gct agc tcc ttt atc aga ggc      880
276 Asp Asp Ile Glu Ser His Val Gly Arg Ala Ser Ser Phe Ile Arg Gly
277         255               260               265
279 gga act gac cag cta caa acc gct cgg gtt tac cag aag aac acg cga      928
280 Gly Thr Asp Gln Leu Gln Thr Ala Arg Val Tyr Gln Lys Asn Thr Arg
281      270               275               280
283 aaa tgg aca tgt att gcc att att att ctc atc atc atc ata act gtt      976
284 Lys Trp Thr Cys Ile Ala Ile Ile Ile Leu Ile Ile Ile Ile Thr Val
285 285               290               295               300
287 gtg gtt ctt gct gtt ttaaaaccgt ggaacaacag cagtggcggc ggcggcggtg     1031
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Input Set : A:\2186PB-1.ST25.txt
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288 Val Val Leu Ala Val
289                 305
291 gtggtggtgg gggtaccact ggaggaagtc aaccaaattc agggacacca ccaaatcctc   1091
293 ctcaggcaag gcgtctattg cgttgaagtt gaagttgaag ttgagtttcg ttatttgcat   1151
295 atatattctt tctttgaaaa accttattat caaaccagct ttgtgttact actttctact   1211
297 gctggtttgt tgttaatctc ccgtttattt ggtttttgtg aaagaattta aaatgtgggt   1271
299 tagatgagaa aattagtaca acattctctt gtatctatgt ttgctaccct gacgtagctc   1331
301 gag                                                                 1334
304 <210> SEQ ID NO: 4
305 <211> LENGTH: 305
306 <212> TYPE: PRT
307 <213> ORGANISM: Arabidopsis thaliana
309 <400> SEQUENCE: 4
311 Met Asn Asp Leu Phe Ser Ser Ser Phe Ser Arg Phe Arg Ser Gly Glu
312 1               5                  10                  15
315 Pro Ser Pro Arg Arg Asp Val Ala Gly Gly Gly Asp Gly Val Gln Met
316             20                  25                  30
319 Ala Asn Pro Ala Gly Ser Thr Gly Gly Val Asn Leu Asp Lys Phe Phe
320          35                  40                  45
323 Glu Asp Val Glu Ser Val Lys Glu Glu Leu Lys Glu Leu Asp Arg Leu
324      50                  55                  60
327 Asn Glu Thr Leu Ser Ser Cys His Glu Gln Ser Lys Thr Leu His Asn
328 65                  70                  75                  80
331 Ala Lys Ala Val Lys Asp Leu Arg Ser Lys Met Asp Gly Asp Val Gly
332              85                  90                  95
335 Val Ala Leu Lys Lys Ala Lys Met Ile Lys Val Lys Leu Glu Ala Leu
336              100                 105                 110
339 Asp Arg Ala Asn Ala Ala Asn Arg Ser Leu Pro Gly Cys Gly Pro Gly
340          115                 120                 125
343 Ser Ser Ser Asp Arg Thr Arg Thr Ser Val Leu Asn Gly Leu Arg Lys
344      130                 135                 140
347 Lys Leu Met Asp Ser Met Asp Ser Phe Asn Arg Leu Arg Glu Leu Ile
348 145                 150                 155                 160
351 Ser Ser Glu Tyr Arg Glu Thr Val Gln Arg Arg Tyr Phe Thr Val Thr
352                  165                 170                 175
355 Gly Glu Asn Pro Asp Glu Arg Thr Leu Asp Arg Leu Ile Ser Thr Gly
356              180                 185                 190
359 Glu Ser Glu Arg Phe Leu Gln Lys Ala Ile Gln Glu Gln Gly Arg Gly
360          195                 200                 205
363 Arg Val Leu Asp Thr Ile Asn Glu Ile Gln Glu Arg His Asp Arg Val
364      210                 215                 220
367 Lys Asp Ile Glu Lys Asn Leu Arg Glu Leu His Gln Val Phe Leu Asp
368 225                 230                 235                 240
371 Met Ala Val Leu Val Glu His Gln Gly Ala Gln Leu Asp Asp Ile Glu
372                  245                 250                 255
375 Ser His Val Gly Arg Ala Ser Ser Phe Ile Arg Gly Gly Thr Asp Gln
376              260                 265                 270
379 Leu Gln Thr Ala Arg Val Tyr Gln Lys Asn Thr Arg Lys Trp Thr Cys
380          275                 280                 285
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VERIFICATION SUMMARY   DATE: 09/03/2002
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Input Set : A:\2186PB-1.ST25.txt
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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date